SEQUENCE LISTING

<110> Endo, Keiji
Ozaki, Katsuya

<120> Modified promoter

<130> 295199US0PCT

<140> 10/589,960
<141> 2006-08-18

<150> PCT/JP05/03757
<151> 2006-03-04

<150> JP 2004-062853
<151> 2004-03-05

<160> 20

<170> PatentIn version 3.3

<210> 1
<211> 572
<212> DNA
<213> Bacillus sp. KSM-S237

<400> 1
gatttgccga tgcaacaggc ttatatttag aggaaatttc tttttaaatt gaatacggaa 60

taaaatcagg taaacaggtc ctgattttat ttttttgagt tttttagaga actgaagatt 120

gaaataaaag tagaagacaa aggacataag aaaattgcat tagttttaat tatagaaaac 180

gccttttttat aattatttat acctagaacg aaaatactgt ttcgaaagcg gtttactata 240

aaaccttata ttccggctct tttttaaaac agggggtaaa aattcactct agtattctaa 300

tttcaacatg ctataataaa tttgtaagac gcaatatgca tctcttttttt tacgatatat 360

gtaagcggtt aaccttgtgc tatatgccga tttaggaagg ggggtagatt gagtcaagta 420

gtaataatat agataactta taagttgttg agaagcagga gagcatctgg gttactcaca 480

agtttttttta aaactttaac gaaagcactt tcggtaatgc ttatgaattt agctatttga 540

ttcaattact ttaaaaatat ttaggaggta at 572

<210> 2
<211> 609
<212> DNA
<213> Bacillus sp. KSM-64

<400> 2
agtacttacc attttagagt caaaagatag aagccaagca ggatttgccg atgcaaccgg 60

cttatattta gagggaattt ctttttaaat tgaatacgga ataaaatcag gtaaacaggt 120

cctgatttta ttttttgaa ttttttgag aactaaagat tgaaatagaa gtagaagaca 180

acggacataa gaaaattgta ttagttttaa ttatagaaaa cgcttttcta taattattta 240

tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc 300

ttttttaaa caggggtga aaattcactc tagtattcta atttcaacat gctataataa 360

atttgtaaga cgcaatatac atctttttt tatgatattt gtaagcggtt aaccttgtgc 420

tatatgccga tttaggaagg gggtagattg agtcaagtag tcataattta gataacttat 480

aagttgttga gaagcaggag agaatctggg ttactcacaa gttttttaaa acattatcga 540

aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta 600

ggaggtaat 609

<210> 3
<211> 3149
<212> DNA
<213> Bacillus sp. KSM-S237

<400> 3
gatttgccga tgcaacaggc ttatatttag aggaaatttc tttttaaatt gaatacggaa 60

taaaatcagg taaacaggtc ctgattttat ttttttgagt tttttagaga actgaagatt 120

gaaataaaag tagaagacaa aggacataag aaaattgcat tagttttaat tatagaaaac 180

gccttttttat aattatttat acctagaacg aaaatactgt ttcgaaagcg gtttactata 240

aaaccttata ttccggctct tttttaaaac agggggtaaa aattcactct agtattctaa 300

tttcaacatg ctataataaa tttgtaagac gcaatatgca tctcttttttt tacgatatat 360

gtaagcggtt aaccttgtgc tatatgccga tttaggaagg ggggtagatt gagtcaagta 420

gtaataatat agataactta taagttgttg agaagcagga gagcatctgg gttactcaca 480

agtttttttta aaactttaac gaaagcactt tcggtaatgc ttatgaattt agctatttga 540

ttcaattact ttaaaaatat ttaggaggta atatgtgtta agaaagaaaa caaagcagtt 600

gatttcttcc attcttattt tagttttact tctatcttta tttccggcag ctcttgcagc 660

agaaggaaac actcgtgaag acaattttaa acatttatta ggtaatgaca atgttaaacg 720

cccttctgag gctggcgcat tacaattaca agaagtcgat ggacaaatga cattagtaga 780

tcaacatgga gaaaaaattc aattacgtgg aatgagtaca cacggattac agtggtttcc 840

tgagatcttg aatgataacg catacaaagc tctttctaac gattgggatt ccaatatgat 900

tcgtcttgct atgtatgtag gtgaaaatgg gtacgctaca aaccctgagt taatcaaaca 960

aagagtgatt gatggaattg agttagcgat tgaaaatgac atgtatgtta ttgttgactg 1020

gcatgttcat gcgccaggtg atcctagaga tcctgtttat gcaggtgcta aagatttctt 1080

tagagaaatt gcagctttat accctaataa tccacacatt atttatgagt tagcgaatga 1140

gccgagtagt aataataatg gtggagcagg gattccgaat aacgaagaag gttggaaagc 1200

ggtaaaagaa tatgctgatc caattgtaga aatgttacgt aaaagcggta atgcagatga 1260

caacattatc attgttggta gtccaaactg gagtcagcgt ccggacttag cagctgataa 1320
tccaattgat gatcaccata caatgtatac tgttcacttc tacactggtt cacatgctgc 1380
ttcaactgaa agctatccgt ctgaaactcc taactctgaa agaggaaacg taatgagtaa 1440
cactcgttat gcgttagaaa acggagtagc ggtatttgca acagagtggg gaacgagtca 1500
agctagtgga gacggtggtc cttactttga tgaagcagat gtatggattg aatttttaaa 1560
tgaaaacaac attagctggg ctaactggtc tttaacgaat aaaaatgaag tatctggtgc 1620
atttacacca ttcgagttag gtaagtctaa cgcaaccaat cttgacccag gtccagatca 1680
tgtgtgggca ccagaagaat taagtctttc tggagaatat gtacgtgctc gtattaaagg 1740
tgtgaactat gagccaatcg accgtacaaa atacacgaaa gtactttggg actttaatga 1800
tggaacgaag caaggatttg gagtgaattc ggattctcca aataaagaac ttattgcagt 1860
tgataatgaa aacaacactt tgaaagtttc gggattagat gtaagtaacg atgtttcaga 1920
tggcaacttc tgggctaatg ctcgtctttc tgccaacggt tggggaaaaa gtgttgatat 1980
tttaggtgct gagaagctta caatggatgt tattgttgat gaaccaacga cggtagctat 2040
tgcggcgatt ccacaaagta gtaaaagtgg atgggcaaat ccagagcgtg ctgttcgagt 2100
gaacgcggaa gattttgtcc agcaaacgga cggtaagtat aaagctggat taacaattac 2160
aggagaagat gctcctaacc taaaaaatat cgcttttcat gaagaagata acaatatgaa 2220
caacatcatt ctgttcgtgg gaactgatgc agctgacgtt atttacttag ataacattaa 2280
agtaattgga acagaagttg aaattccagt tgttcatgat ccaaaaggag aagctgttct 2340
tccttctgtt tttgaagacg gtacacgtca aggttgggac tgggctggag agtctggtgt 2400
gaaaacagct ttaacaattg aagaagcaaa cggttctaac gcgttatcat gggaatttgg 2460
atatccagaa gtaaaaccta gtgataactg ggcaacagct ccacgtttag atttctggaa 2520
atctgacttg gttcgcggtg agaatgatta tgtagctttt gatttctatc tagatccagt 2580
tcgtgcaaca gaaggcgcaa tgaatatcaa tttagtattc cagccaccta ctaacgggta 2640
ttgggtacaa gcaccaaaaa cgtatacgat taactttgat gaattagagg aagcgaatca 2700
agtaaatggt ttatatcact atgaagtgaa aattaacgta agagatatta caaacattca 2760
agatgacacg ttactacgta acatgatgat cattttgca gatgtagaaa gtgactttgc 2820
agggagagtc tttgtagata atgttcgttt tgaggggct gctactactg agccggttga 2880
accagagcca gttgatcctg gcgaagagac gccacctgtc gatgagaagg aagcgaaaaa 2940
agaacaaaaa gaagcagaga aagaagagaa agaagcagta aaagaagaaa agaaagaagc 3000
taaagaagaa aagaaagcag tcaaaaatga ggctaagaaa aaataatcta ttaaactagt 3060
tatagggtta tctaaaggtc tgatgtagat cttttagata acctttttct tgcataactg 3120
gacacagagt tgttattaaa gaaagtaag 3149

<210> 4
<211> 795
<212> PRT
<213> Bacillus sp. KSM-S237

<400> 4

Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn
1 5 10 15

Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu
20 25 30

Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
35 40 45

Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
50 55 60

Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met
65 70 75 80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro
85 90 95

Glu Leu Ile Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu
100 105 110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
115 120 125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile
130 135 140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145 150 155 160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
165 170 175

Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
180 185 190

Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
195 200 205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
210 215 220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225 230 235 240

Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly
245 250 255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
260 265 270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro
275 280 285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
290 295 300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305 310 315 320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp
325 330 335

Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly
340 345 350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
355 360 365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
370 375 380

Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala
385 390 395 400

Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser
405 410 415

Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala
420 425 430

Asn Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr
435 440 445

Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile
450 455 460

Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg

465 470 475 480

Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala
485 490 495

Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala
500 505 510

Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly
515 520 525

Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly
530 535 540

Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val
545 550 555 560

Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala
565 570 575

Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly
580 585 590

Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser
595 600 605

Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu
610 615 620

Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro
625 630 635 640

Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro
645 650 655

Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn
660 665 670

Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr
675 680 685

Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr
690 695 700

Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe
705 710 715 720

Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr
725 730 735

Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro
740 745 750

Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys
755 760 765

Glu Glu Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu
770 775 780

Lys Lys Ala Val Lys Asn Glu Ala Lys Lys Lys
785 790 795

<210> 5
<211> 3332
<212> DNA
<213> Bacillus sp. KSM-64

<400> 5
agtacttacc attttagagt caaaagatag aagccaagca ggatttgccg atgcaaccgg 60

cttatattta gagggaattt ctttttaaat tgaatacgga ataaaatcag gtaaacaggt 120

cctgatttta ttttttttgaa ttttttttgag aactaaagat tgaaatagaa gtagaagaca 180

acggacataa gaaaattgta ttagttttaa ttatagaaaa cgcttttcta taattattta 240

tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc 300

ttttttttaaa caggggggtga aaattcactc tagtattcta atttcaacat gctataataa 360

atttgtaaga cgcaatatac atctttttttt tatgatattt gtaagcggtt aaccttgtgc 420

tatatgccga tttaggaagg gggtagattg agtcaagtag tcataattta gataacttat 480

aagttgttga gaagcaggag agaatctggg ttactcacaa gttttttaaa acattatcga 540

aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta 600

ggaggtaata tgatgttaag aaagaaaaca aagcagttga tttcttccat tcttatttta 660

gttttacttc tatctttatt tccgacagct cttgcagcag aaggaaacac tcgtgaagac 720

aattttaaac atttattagg taatgacaat gttaaacgcc cttctgaggc tggcgcatta 780

caattacaag aagtcgatgg acaaatgaca ttagtagatc aacatggaga aaaaattcaa 840

ttacgtggaa tgagtacaca cggattacaa tggtttcctg agatcttgaa tgataacgca 900

tacaaagctc ttgctaacga ttgggaatca aatatgattc gtctagctat gtatgtcggt 960

gaaaatggct atgcttcaaa tccagagtta attaaaagca gagtcattaa aggaatagat 1020

cttgctattg aaaatgacat gtatgtcatc gttgattggc atgtacatgc acctggtgat 1080

cctagagatc ccgtttacgc tggagcagaa gatttcttta gagatattgc agcattatat 1140

cctaacaatc cacacattat ttatgagtta gcgaatgagc caagtagtaa caataatggt 1200
ggagctggga ttccaaataa tgaagaaggt tggaatgcgg taaaagaata cgctgatcca 1260
attgtagaaa tgttacgtga tagcgggaac gcagatgaca atattatcat tgtgggtagt 1320
ccaaactgga gtcagcgtcc tgacttagca gctgataatc caattgatga tcaccataca 1380
atgtatactg ttcacttcta cactggttca catgctgctt caactgaaag ctatccgcct 1440
gaaactccta actctgaaag aggaaacgta atgagtaaca ctcgttatgc gttagaaaac 1500
ggagtagcag tatttgcaac agagtgggga actagccaag caaatggaga tggtggtcct 1560
tactttgatg aagcagatgt atggattgag tttttaaatg aaaacaacat tagctgggct 1620
aactggtctt taacgaataa aaatgaagta tctggtgcat ttacaccatt cgagttaggt 1680
aagtctaacg caacaagtct tgacccaggg ccagaccaag tatgggtacc agaagagtta 1740
agtctttctg gagaatatgt acgtgctcgt attaaaggtg tgaactatga gccaatcgac 1800
cgtacaaaat acacgaaagt actttgggac tttaatgatg gaacgaagca aggatttgga 1860
gtgaatggag attctccagt tgaagatgta gttattgaga atgaagcggg cgctttaaaa 1920
ctttcaggat tagatgcaag taatgatgtt tctgaaggta attactgggc taatgctcgt 1980
ctttctgccg acggttgggg aaaaagtgtt gatattttag gtgctgaaaa acttactatg 2040
gatgtgattg ttgatgagcc gaccacggta tcaattgctg caattccaca agggccatca 2100
gccaattggg ttaatccaaa tcgtgcaatt aaggttgagc caactaattt cgtaccgtta 2160
ggagataagt ttaaagcgga attaactata acttcagctg actctccatc gttagaagct 2220
attgcgatgc atgctgaaaa taacaacatc aacaacatca ttctttttgt aggaactgaa 2280
ggtgctgatg ttatctattt agataacatt aaagtaattg gaacagaagt tgaaattcca 2340
gttgttcatg atccaaaagg agaagctgtt cttccttctg tttttgaaga cggtacacgt 2400
caaggttggg actgggctgg agagtctggt gtgaaaacag ctttaacaat tgaagaagca 2460
aacggttcta acgcgttatc atgggaattt ggatacccag aagtaaaacc tagtgataac 2520
tgggcaacag ctccacgttt agatttctgg aaatctgact tggttcgcgg tgaaaatgat 2580
tatgtaactt ttgatttcta tctagatcca gttcgtgcaa cagaaggcgc aatgaatatc 2640
aatttagtat tccagccacc tactaacggg tattgggtac aagcaccaaa aacgtatacg 2700
attaactttg atgaattaga ggaagcgaat caagtaaatg gtttatatca ctatgaagtg 2760
aaaattaacg taagagatat tacaaacatt caagatgaca cgttactacg taacatgatg 2820
atcatttttg cagatgtaga aagtgacttt gcagggagag tctttgtaga taatgttcgt 2880
tttgaggggg ctgctactac tgagccggtt gaaccagagc cagttgatcc tggcgaagag 2940
acgccgcctg tcgatgagaa ggaagcgaaa aaagaacaaa aagaagcaga gaaagaagag 3000

aaagaagcag taaaagaaga aaagaaagaa gctaaagaag aaaagaaagc aatcaaaaat 3060

gaggctacga aaaaataatc taataaacta gttatagggt tatctaaagg tctgatgcag 3120

atcttttaga taacctttt ttgcataact ggacatagaa tggttattaa agaaagcaag 3180

gtgtttatac gatattaaaa aggtagcgat tttaaattga aacctttaat aatgtcttgt 3240

gatagaatga tgaagtaatt taagaggggg aaacgaagtg aaaacggaaa tttctagtag 3300

aagaaaaaca gaccaagaaa tactgcaagc tt 3332

<210> 6
<211> 793
<212> PRT
<213> Baccillus sp. KSM-64

<400> 6

Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn
1 5 10 15

Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu
20 25 30

Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
35 40 45

Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
50 55 60

Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
65 70 75 80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
85 90 95

Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
100 105 110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
115 120 125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
130 135 140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145 150 155 160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
165 170 175

```
Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
            180                 185                 190

Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
        195                 200                 205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
    210                 215                 220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225                 230                 235                 240

Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
                245                 250                 255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
            260                 265                 270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
        275                 280                 285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
    290                 295                 300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305                 310                 315                 320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp
                325                 330                 335

Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly
            340                 345                 350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
        355                 360                 365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
    370                 375                 380

Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile
385                 390                 395                 400

Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn
                405                 410                 415

Asp Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp
            420                 425                 430
```

Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met
435 440 445

Asp Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro
450 455 460

Gln Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val
465 470 475 480

Glu Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu
485 490 495

Thr Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His
500 505 510

Ala Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu
515 520 525

Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu
530 535 540

Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro
545 550 555 560

Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu
565 570 575

Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn
580 585 590

Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn
595 600 605

Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg
610 615 620

Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg
625 630 635 640

Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr
645 650 655

Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp
660 665 670

Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val

675 680 685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
690 695 700

Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly
705 710 715 720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
725 730 735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
740 745 750

Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu
755 760 765

Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys
770 775 780

Ala Ile Lys Asn Glu Ala Thr Lys Lys
785 790

<210> 7
<211> 572
<212> DNA
<213> Bacillus sp. KSM-S237

<400> 7
gatttgccga tgcaacaggc ttatatttag aggaaatttc tttttaaatt gaatacggaa 60

taaaatcagg taaacaggtc ctgattttat ttttttgagt tttttagaga actgaagatt 120

gaaataaaag tagaagacaa aggacataag aaaattgcat tagttttaat tatagaaaac 180

gccttttttat aattatttat acctagaacg aaaatactgt ttcgaaagcg gtttactata 240

aaaccttata ttccggctct tttttaaaac agggggtaaa aattcactct agtattctaa 300

tttcaacatg ctataataaa tttgtaagac gcaatatgca tctcttttttt tacgatatat 360

gtaagcggtt aaccttgtgc tatatgccga tttaggaagg ggggtagaat atttcaagta 420

gtaataacat acaatactta taagttgttg agaagcagga gagcatctgg gttactcaca 480

agtttttttta aaactttaac gaaagcactt tcggtaatgc ttatgaattt agctatttga 540

ttcaattact ttaaaaatat ttaggaggta at 572

<210> 8
<211> 609
<212> DNA
<213> Bacillus sp. KSM-64

<400> 8
agtacttacc attttagagt caaaagatag aagccaagca ggatttgccg atgcaaccgg 60

cttatattta gagggaattt ctttttaaat tgaatacgga ataaaatcag gtaaacaggt 120

cctgatttta ttttttgaa ttttttgag aactaaagat tgaaatagaa gtagaagaca 180

acggacataa gaaaattgta ttagttttaa ttatagaaaa cgcttttcta taattattta 240

tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc 300

ttttttaaa caggggtga aaattcactc tagtattcta atttcaacat gctataataa 360

atttgtaaga cgcaatatac atctttttt tatgatattt gtaagcggtt aaccttgtgc 420

tatatgccga tttaggaagg gggtagaata tttcaagtag taataacata caatacttat 480

aagttgttga gaagcaggag agaatctggg ttactcacaa gtttttaaa acattatcga 540

aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta 600

ggaggtaat 609

<210> 9
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase; the sequece with a insertion of the BamHI restriction site at the 5'-end

<400> 9
ttgcggatcc aacaggctta tatttagagg aaatttc 37

<210> 10
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase; the sequence containing eight nucleotides substitution for SigmaE recognition

<400> 10
gtatgttatt actacttgaa atattctacc ccccttccta 40

<210> 11
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase; the sequence containing eight nucleotides substitution for SigmaE recognition

<400> 11

atatttcaag tagtaataac atacaatact tataagttg 39

<210> 12
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase

<400> 12
tcgctaccct tttattatcg 20

<210> 13
<211> 1795
<212> DNA
<213> Bacillus sp. KSM-K38

<400> 13
caggccagcc aaagtagcca ccaactaagt aacatcgatt caggataaaa gtatgcgaaa 60

cgatgcgcaa aactgcgcaa ctactagcac tcttcaggga ctaaaccacc ttttttccaa 120

aaatgacatc atataaacaa atttgtctac caatcactat ttaaagctgt ttatgatata 180

tgtaagcgtt atcattaaaa ggaggtattt gatgagaaga tgggtagtag caatgttggc 240

agtgttattt ttatttcctt cggtagtagt tgcagatgga ttgaacggta cgatgatgca 300

gtattatgag tggcatttgg aaaacgacgg gcagcattgg aatcggttgc acgatgatgc 360

cgcagctttg agtgatgctg gtattacagc tatttggatt ccgccagcct acaaaggtaa 420

tagtcaggcg gatgttgggt acggtgcata cgatctttat gatttaggag agttcaatca 480

aaagggtact gttcgaacga aatacggaac taaggcacag cttgaacgag ctattgggtc 540

ccttaaatct aatgatatca atgtatacgg agatgtcgtg atgaatcata aaatgggagc 600

tgattttacg gaggcagtgc aagctgttca agtaaatcca acgaatcgtt ggcaggatat 660

ttcaggtgcc tacacgattg atgcgtggac gggtttcgac ttttcagggc gtaacaacgc 720

ctattcagat tttaagtgga gatggttcca ttttaatggt gttgactggg atcagcgcta 780

tcaagaaaat catattttcc gctttgcaaa tacgaactgg aactggcgag tggatgaaga 840

gaacggtaat tatgattacc tgttaggatc gaatatcgac tttagtcatc cagaagtaca 900

agatgagttg aaggattggg gtagctggtt taccgatgag ttagatttgg atggttatcg 960

tttagatgct attaaacata ttccattctg gtatacatct gattgggttc ggcatcagcg 1020

caacgaagca gatcaagatt tatttgtcgt aggggaatat tggaaggatg acgtaggtgc 1080

tctcgaattt tatttagatg aaatgaattg ggagatgtct ctattcgatg ttccacttaa 1140

ttataatttt taccgggctt cacaacaagg tggaagctat gatatgcgta atattttacg 1200

aggatcttta gtagaagcgc atccgatgca tgcagttacg tttgttgata atcatgatac 1260

tcagccaggg gagtcattag agtcatgggt tgctgattgg tttaagccac ttgcttatgc 1320

gacaattttg acgcgtgaag gtggttatcc aaatgtattt tacggtgatt actatgggat 1380

tcctaacgat aacatttcag ctaaaaaaga tatgattgat gagctgcttg atgcacgtca 1440

aaattacgca tatggcacgc agcatgacta ttttgatcat tgggatgttg taggatggac 1500

tagggaagga tcttcctcca gacctaattc aggccttgcg actattatgt cgaatggacc 1560

tggtggttcc aagtggatgt atgtaggacg tcagaatgca ggacaaacat ggacagattt 1620

aactggtaat aacggagcgt ccgttacaat taatggcgat ggatggggcg aattctttac 1680

gaatggagga tctgtatccg tgtacgtgaa ccaataacaa aaagccttga gaagggattc 1740

ctccctaact caaggctttc tttatgtcgc ttagctttac gcttctacga ctttg 1795

<210> 14
<211> 480
<212> PRT
<213> Bacillus sp. KSM-K38

<400> 14

Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
1 5 10 15

Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

```
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145                 150                 155                 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
                165                 170                 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
            180                 185                 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
        195                 200                 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
    210                 215                 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225                 230                 235                 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
                245                 250                 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
            260                 265                 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
        275                 280                 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
    290                 295                 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305                 310                 315                 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
                325                 330                 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
            340                 345                 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
        355                 360                 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
    370                 375                 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385                 390                 395                 400
```

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
450 455 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465 470 475 480

<210> 15
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase; the sequece with a insertion of the BamHI restriction site at the 5'-end

<400> 15
cccggatcca acaggcttat attta 25

<210> 16
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase and its 5'-portion designed from nucleotide sequence of Bacillus sp. KSM-K38 gene for amylase

<400> 16
ttcaatccat ctgctgcaag agctgccgg 29

<210> 17
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucle otide sequence of Bacillus sp. KSM-K38 gene for amylase and its 5'-portion designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase

<400> 17
gctcttgcag cagatggatt gaacggtacg 30

<210> 18
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of Bacillus sp. KSM-K38 gene for amylase; the sequece with a insertion of the XbaI restriction site at the 5'-end

<400> 18
ttggtctaga ccccaagctt caaagtcgta 30

<210> 19
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> A promoter sequence recognized by SigE

<400> 19
atatttcaag tagtaataac atacaat 27

<210> 20
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Original sequence in an alkaline cellulase gene

<400> 20
ttgagtcaag tagtaataat atagata 27